DRAFTSMAN

DOWELEND "DYEVOO

CLASS SUBCLASS

1/3

ovary

liver

muscle

testis

spleen

intestine

pancreas

seminal vesicle

kidney

brain

thymus

lung

heart

FIG. 1

2/3

1	CGGGCCAGGAGGACGCCCACCTGTGAGCCTGCGACCCCCTTATGTTGCAGGCGAGAC														60						
-	R	Α	R	R	R	T	P	T	C	E	·P	A.	T	P	L	C	C	R	R	D	
61	R A R R R T P T C E P A T P L C C R R D CATTACGTAGACTTCCAGGAACTGGGATGGCGGGACTGGATACTGCAGCCCGAGGGGTAC H Y V D F Q E L G W R D W I L Q P E G Y													120							
	ч	Y	v	D	F	0	E	L	G	W.	R	D	W	I	L	Q	P	E	G	Y	
121	CAGCTGAATTACTGCAGTGGGCAGTGCCTCCCCACCTGGCTGG												180								
	Q	L	N	Y	C	S	G	Q	C	P	P	H	L	λ	G	S	P	G	I	A	240
181	GCCTCTTTCCATTCTGCCGTCTTCAGCCTCCTCAAAGCCAACAATCCTTGGCCTGCCAGT A S F H S A V F S L L K A N N P W P A S												240								
	A	s	F	H	S	A	V	F	, S	L,	L,	K	A	N	N	P	W	P	A	S	300
241	AC	CTC	CTC	TIC	TCI	rccc	TAC	TIC	ccc	AAC	CCC		CIC	TCI	CCI	CIA	CC1	GGA	VICA	TAAT	300
	T	S	C	С	V	P	T	A	R	R	P	L	S	L	L	Y	L	D	H	N	360
301	GC	CAA	TGI	CGI	CA	AGAC	:GG1	ATG!	<i>L</i> CCC	LAGA	TAT	(GC)	CCI	CG	rege 7	CIC.	rige C	CIC	CAU	CTAG	360

FIG. 2

Family member	% identity with GDF-12
GDF-1	43
GDF-3	36
GDF-5	36
GDF-6	39 42
GDF-7	30
GDF-9 BMP-3	37
BMP-2	43
BMP-4	42
Vgr-1	41
OP-1	40
BMP-5	38
OP-2	39
MIS	30
Inhibin-a	27
Inhibin-BA	47
Inhibin-BB	50
Nodal	38 21
GDNF	36
TGF-B1 TGF-B2	36
TGF-B3	41
101-03	- 7

FIG. 4

DARKEL IN THE SECTION OF THE SECTION

·.	APPROVED	O.G. FIG.						
	BA	CLASS	SUBCLASS					
	erafteman							

an l		
•	GAGCTGTGAGGGTCAAGCACAGCTATCCATCAGATGATCTACTTTCAGCCTTCCTGAGTC	60 3/3
1 61	CAGACAATAGAAGACAGGTGGCTGTACCCTTGGCCAAGGGTAGGTGTGGCAGTGGTGTC	120
121	TGCTGTCACTGTGCCCTCATTGGCCCCCAGCAATCAGACTCAACAGACGGAGCAACTGCC	180
181	ATCCGAGGCTCCTGAACCAGGGCCATTCACCAGGAGCATGCGGCTCCCTGATGTCCAGCT	240
101	M R L P D V O L	240
241	CTGGCTGGTGCTGTGGGCACTGGTGCGAGCACAGGGGACAGGGTCTGTGTGTCCCTC	300
	W L V L L W A L V R A O G T G S V C P S	
301	CTGTGGGGGCTCCAAACTGGCACCCCAAGCAGAACGAGCTCTGGTGCTGGAGCTAGCCAA	360
	C G G S K L A P Q A E R A L V L E L A K	
361	GCAGCAAATCCTGGATGGGTTGCACCTGACCAGTCGTCCCAGAATAACTCATCCTCCACC	420
	QQILDGLHLTSRPRITHPP	
421	CCAGGCAGCGCTGACCAGAGCCCTCCGGAGACTACAGCCAGGGAGTGTGGCTCCAGGGAA	480
	Q A A L T R A L R R L Q P G S V A P G N	
481	TGGGGAGGAGGTCATCAGCTTTGCTACTGTCACAGACTCCACTTCAGCCTACAGCTCCCT	540
	G E E V I S F A T V T D S T S A Y S S L	
541	GCTCACTTTTCACCTGTCCACTCCTCGGTCCCACCACCTGTACCATGCCCGCCTGTGGCT	600
	LTFHLSTPRSHHLYHARLWL	
601	GCACGTGCTCCCCACCCTTCCTGGCACTCTTTGCTTGAGGATCTTCCGATGGGGACCAAG	660
	HVLPTLPGTLCLRIFRWGPR	
661	GAGGAGGCGCCAAGGGTCCCGCACTCTCCTGGCTGAGCACCACATCACCAACCTGGGCTG	720
	RRRQGSRTLLAEHHITNLGW	
721	GCATACCTTAACTCTGCCCTCTAGTGGCTTGAGGGGTGAGAAGTCTGGTGTCCTGAAACT	780
	H T L T L P S S G L R G E K S G V L K L	
781	GCAACTAGACTGCAGACCCCTAGAAGG <u>CAACAGCA</u> CAGTTACTGGACAACCGAGGCGGCT	840
	Q L D C R P L E G N S T V T G Q P R R L	
841	CTTGGACACAGCAGCACCAGCAGCCCTTCCTAGAGCTTAAGATCCGAGCCAATGAGCC	900
	LDTAGHQQPFLELKIRANEP	
901	TGGAGCAGGCCGGCCAGGAGGAGGACCCCCACCTGTGAGCCTGCGACCCCCTTATGTTG	960
	GAGRAR TPTCEPATPLCC	
961	CAGGCGAGACCATTACGTAGACTTCCAGGAACTGGGATGGCGGGACTGGATACTGCAGCC	1020
	RRDHYVDFQELGWRDWILQP	
1021	CGAGGGGTACCAGCTGAATTACTGCAGTGGGCAGTGCCCTCCCCACCTGGCTGG	1080
	E G Y Q L N Y C S G Q C P P H L A G S P	
1081	AGGCATTGCTGCCTCTTTCCATTCTGCCGTCTTCAGCCTCCTCAAAGCCAACAATCCTTG	1140
1141	GIAASFHSAVFSLLKANNPW	1200
1141	GCCTGCCAGTACCTCTGTTGTGTCCCTACTGCCCGAAGGCCCCTCTCTCT	1200
1201	PASTSCCVPTARPLSLLYL GGATCATAATGGCAATGTGGTCAAGACGGATGTGCCAGATATGGTGGAGGCCTGTGG	1260
1201		1260
1261	D H N G N V V K T D V P D M V V E A C G CTGCAGCTAGCAAGAGACCTGGGGCTTTGGAGTGAAGACCAAGATGAAGTTTCCCAG	1220
1201	C S *	1320
1321	GCACAGGGCATCTGTGACTGGAGGCATCAGATTCCTGATCCACACCCCAACCCAACAACC	1200
1321	ACCTGGCAATATGACTCACTTGACCCCTATGGGACCCAAATGGGCACTTTCTTGTCTGAG	1380
1441	ACTOTOGOTTATTCCAGGTTGGCTGATGTGTTGGGAGATGGGTAAAGCGTTTCTTCTAAA	1440 1500
1501	GGGGTCTACCCAGAAAGCATGATTTCCTGCCCTAAGTCCTGTGAGAAGATGTCAGGGACT	1560
1561	AGGGAGGGAGGGAAGGCAGAGAAAAATTACTTAGCCTCTCCCAAGATGAGAAAGTC	1620
1621	CTCAAGTGAGGGAGGAGGAAGCAGATAGATGGTCCAGCAGGCTGAAGCAGGGTAAGCA	1680
1681	GGCTGGCCCAGGGTAAGGGCTGTTGAGGTACCTTAAGGGAAGGTCAAGAGGGAAGATGGGC	1740
1741	AAGGCGCTGAGGAGGATGCTTAGGGGACCCCCAGAAACAGGAGTCAGGAAAATGAGGCA	1800
1801	CTAAGCCTAAGAAGTTCCCTGGTTTTTCCCAGGGGACAGGACCCACTGGGAGACAAGCAT	1860
1861	TTATACTTTCTTCTTTTTTTTTTTTTTTGAGATCGAGTCTCGCTCTGTCACCAGGCT	1920
1921	GGAGTGCAGTGACACGATCTTGGCTCACTGCAACCTCCGTCTCCTGGGTTCAAGTGATTC	1980
1981	TTCTGCCTCAGCCTCCCGAGCAGCTGGGATTACAGGCGCCCACTAATTTTTGTATTCTTA	2040
2041	GTAGAAACGAGGTTTCAACATGTTGGCCAGGATGGTCTCAATCTCTTGACCTCTTGATCC	2100
2101	ACCCGACTTGGCCTCCCGAAGTGATGAGATTATAGGCGTGAGCCACCGCGCCTTGCTTAT	2160
2161	ACTTTCTTAATAAAAGGAGAAAGAAAATCAACAAATGTGAGTCATAAAGAAGGGTTAGG	2220
2221	GTGATGGTCCAGAGCAACAGTTCTTCAAGTGTACTCTGTAGGCTTCTGGGAGGTCCCTTT	2280
2281	TCAGGGGTGTCCACAAAGTCAAAGCTATTTTCATAATAATACTAACATGTTATTTGCCTT	2340
2341	TTGAATTCTCATTATCTTAAAATTGTATTGTGGAGTTTTCCAGAGGCCGTGTGACATGTG	2400
2401	ATTACATCATCTTTCTGAC 2419	